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Sequence:

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Database

Result No.

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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiAccession: 840367
Riklein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;fitle: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MuID:94080891; PMID:8258341
A;Reterence number: 840367
A;Reterence proper mRNA
A;Residues: 1-127 <KLE>
A;Residues: 1-127 <KLE>
A;Residues: 1-127 <KLE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterzamer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gy kappa chain - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Accession: S40331
R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: S40312; MuID: 94080891; PMID: 8258341
A; Accession: S40331
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-123 «KLB.
A; Cross-references: EMBL: X72441; NID: 9441350; PIDN: CAA51109.1; PID: 9441351
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 32-106/ Domain: immunoglobulin homology < IMM>
kappa chain - h
kappa chain V-J
kappa chain V-I
kappa chain - h
J lambda chain V
Ig kappa chain - h
Ig kappa chain V-J
Ig kappa chain V-I
Ig hambda chain V
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Ig kappa chain V-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.6%; Score 498; DB 2; Length 12 ilarity 85.1%; Pred. No. 1.3e-36; Conservative 8; Mismatches 5; Indels
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K1HUAU
K1HUBN
K1HULY
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                                 XIHUOU
S40368
S36275
JL0139
S32001
S31983
S46372
S31977
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Matches
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1545.812 Million cell updates/sec
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                                                                                                                                                                                                       596
1 DIQLTQSPSSLSASVGDRVT.....SHEDPYTFGQGTKVEIKRTV 114
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                                                                                                                     3, 2005, 08:53:28 ; Search time 7.09576 Seconds
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                             283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Ig kappa chain V-J region (T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46370; S984, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reash A;Reference number: S46369; MUID:94313975; PMID:8039491
                                                                                                                                                                                                                                                                                                                                         A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re A; Reference number: $44105
                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-412
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
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Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: EMBL:227171, NID:g415957, PIDN:CAA01695.1, PID:g415958 C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Reywords: heterotetramer; immunoglobulin C,Keywords: heterotetramer; immunoglobulin P;26-100/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAAB3265.1; PID:g940533 C;Superfamily: immunoglobulin V reggion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-90/Domain: immunoglobulin homology < IMM>
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4,
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No. 3.4e-34; Indels
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Pred. No. 2.5e-34;
7; Mismatches 8;
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Local Similarity 81.6%;
les 93; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
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A; Residues: 1-120 <BEN>
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Datession: B49047
R.Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
R.Victor, T.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
A.Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A.Reference number: A49047; MUID:92387224; PMID:1516616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S31998
R; Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A; Description: Lack of promiscuity in autoantigen-specific H and L chain combinations A; Reference number: S31977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                        17 DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQQKPGKAPKULIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLWWYQQKPGKAPKLLIYAASSLQS
                                                                                     1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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A;Experimental source: thymic B lymphocytes
A;Experimental source: thymic B lymphocytes
A;Experimental source: thymic B lymphocytes
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIKR 108
                                                                                                                                                                                                    61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIK 111
                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYXCQQSYSTPRTFGGGTKVEIK 123
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     Pred. No. 1.2e-35;
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                             5; Mismatches
  86.58;
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     Best Local Similarity 86.5
Matches 96; Conservative
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A;Molecule type: nucleic acid
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Matches 91; Conserv
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A, Note: the C region of this chain has the Inv (3) marker R; Steiner, V.; Chang, J.Y.
FRBS Lett. 222, 6-10, 1987
A, Title: Chemical modification of the carboxyl groups of protein substrates enhances their A; Reference number: S02572; MUID: 88005152; PMID: 3115831
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp
C;Complex: an immunoglobulin heterotetramer; such as IgA and IgM, the subunits associate into lan
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IVM>
F;16-90/Domain: immunoglobulin homology <IVM>
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J. Mol. Biol. 222, 581-597, 1991
A.Fille: By-passing immunization. Human antibodies from V-gene libraries displayed on pha A; Reference number: S19663; MUID:92085276; PMID:1748994
A; Accession: S19674
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
                                                                                                                                                                                                                                                 16 DIQMTQSPSSLSASVGDRVTFTCRSSQTI----GTYLNWYQQKPGQAPKLLIFAASSLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                   1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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                                                                                                               Length 125;
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81.2%; Pred. No. 1e-33;
ive 10; Mismatches 7; Indels
  C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;31-105/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                 Indels
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R;Watanabe, S.; Hilschmann, N.
A;Title: The primary structure of a monoclonal kappa-type
A;Reference number: A01868; MUID:71032830; PMID:4097974
A;Accession: A01868
                                                                                                         ; Score 465.5; DB 2;
; Pred. No. 8.8e-34;
11; Mismatches 7;
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A,Residues: 1-108 <WAT>
A,Cross-references: UNIPROT:P01600
                                                                                                            78.1%;
                                                                                                                                                                 91; Conservative
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R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47182
A;Accession: S47182
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
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R; Portcolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A; Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as A; Reference number: S31977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X79786; NID:g506422; PIDN:CAA56182.1; PID:g506423 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLAWYQQKPGKAPKLLIYAASYLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 109;
4.6e-34;
thes 9; Indels
                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
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                                                                                                                                                                                                                                                                                                                                                   78.7%; Score 469; DB 2;
82.1%; Pred. No. 3.8e-34;
iive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 78.5%; Score 468; DB 1 Similarity 79.6%; Pred. No. 4.6e 90; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: $40315
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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Best Local Similarity 82.15
Marches 92; Conservative
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A; Residues: 1-109 < POR>
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Best Local (
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A; Molecule type: mRNA

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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                   1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                              1 EIVLTQSPSSLSASVGDRVTITCRASQSI----SNYLNWYQQKPGKAPKLLIYAASTLQS
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             A;Cross_references: EMBL;X61642; NID:937860; PIDN:CAA43823.1; PID:91335386 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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R.Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1991
A,Title: Expressed human immunoglobulin chi genes and their hypermutation.
A,Reference number: 840312; MUID:94080891; PMID:8258341
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1988
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40370
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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                                                                                                                                                      77.5%; Score 462; DB 2; Length 108; 81.2%; Pred. No. 1.5e-33;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
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79.8%; Pred. No. 1.9e-33;
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                                                                                                 F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                           91; Conservative
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nes 92; Conserv
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Best Local Similarity
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A;Residues: 1-108 <MAR>
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Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C;Acceson: S;2792
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-?
A;Reference number: S52792
A;Accession: S52792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CJACCESSION: S52793

R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995

A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-?

A;Reference number: S52789
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C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
                                                                                           22 DIQLIQSPSFLSASIGDRVTITCRASQGI----NSYLAWYQQKPGKAPKLLIYVASTLQS
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                                                        1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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C;Superfamily: immunoglobulin V reggion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <1MM>
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                                                                                                                                                                                                            78 GVPSRFSGSGSGTEFTLTISSLQPEDFASYXCQQFNSYPFTFGGGTKVEIRRTV 131
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9; Indels
   Mismatches
   10;
   91; Conservative
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A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
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A,Molecule type: mRNA
A,Residues: 1-129 <ROC>
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Search completed: June 3, 2005, 09:17:50 Job time: 8.09576 secs

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OM protein - protein search, using sw model

3, 2005, 08:31:37; Search time 32.7497 Seconds (without alignments) 1782.523 Million cell updates/sec

June

Run on:

US-10-791-619-8 596 1 DIQLTQSPSSLSASVGDRVT.....SHEDPYTFGQGTKVEIKRTV 114 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	Q6gmx8	Q9u177	Q6gmw1	Q968a9	Q6gmx0	Q6pih7	P01600	P01597	P04431	P01606	Q7z3y4	P01594	P04430	09u181	P01605	Q9u170	Q72473	P01665	P01603	P01607	P01611	Q6gmx9	P01598	P01599	P80362	P01667	P01608	P01666	06pit5	P01610	P01664
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SUMMARIES	;	ΩI	Q6GMX8	09UL77	Q6GMW1	Q96SA9	Q6GMX0	Q6PIH7	KV1H HUMAN	KV1E HUMAN	KV1W HUMAN	KV1N HUMAN	Q7Z3 <u>Y</u> 4	KV1B_HUMAN	KV1V HUMAN	Q9UL81	KV1M HUMAN	09UL70	Q7Z473	KV3M MOUSE	KV1K HUMAN	KV10 HUMAN	KV1S HUMAN	Q6GMX9	KV1F HUMAN	KV1G HUMAN	KV1Y HUMAN	KV30 MOUSE	KV1P HUMAN	KV3N MOUSE	QEPITS	KV1R_HUMAN	KV3L_MOUSE
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		Match Length	236	108	236	107	236	236	108	108	129	108	236	108	108	107	108	108			108	108	108	236	108	108	108	111	108	111	236	108	111
	Query	Match	80.7	80.5	78.9	78.6	78.2	78.0	77.9	76.5	76.0	75.5	74.8	74.7	74.7	74.4	74.3	74.2	74.2	74.0	73.8	73.8	73.5			73.2			72.8	72.8	72.8	72.7	72.7
		Score	481	480	470	468.5	466	465	464	456	453	450	446	445	445	443.5	443	442	442	441	440	440	438	437	436	436	436	436	434	434	434	433	433
	Result	No.	7	N	m	4	2	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

P01669 mus musculu Q9ul79 homo sapien P01604 homo sapien G6pih4 homo sapien Q65zc8 homo sapien P01593 homo sapien P01595 homo sapien P01610 homo sapien P01609 homo sapien P01609 homo sapien P01609 homo sapien P01609 homo sapien P01595 homo sapien P01595 homo sapien P01595 homo sapien
KV3Q MOUSE Q9UL79 KV1L HUMAN Q6FIF4 Q96FF6 Q96FC8 KV1D HUMAN KV1D HUMAN KV1D HUMAN KV3H MOUSE Q65ZC9 Q65ZC9 KV1C HUMAN
4040004444
1111 236 236 1108 1116 1007 1111 1111 108
72.3 72.3 72.0 71.6 71.6 71.3 71.2 71.1 71.0 70.8
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ALIGNMENTS

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Generation and initial analysis of more than 15,000 full-length human
                                        TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 82.3
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
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                                                                                                              1 DIQMIQSPSSLSASVGDRVTITCRASQSI----SSYLAWYQQKPGKAPNLLIYAASSLQS
                                                                                             1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                     Gaps
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wh X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.5%; Score 480; DB 2; Length 108; Best Local Similarity 83.9%; Pred. No. 3.3e-40; Matches 94; Conservative 7; Mismatches 7; Indels
                                       Length 236;
                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                            80.7%; Score 481; DB 2; Length 23
82.5%; Pred. No. 6.3e-40;
Mismatches 7; Indels
Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                 108 AA.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SMO0406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF035037; AAD56273.1;
PIR; B49047; B49047.
PIR; S34083; S34083.
                                                                  Matches 94; Conservative
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                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                (Fragment)
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                                                                                                                      23
                                          Query Match
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Q9UL77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLESG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
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01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
TISSUE=Spieen;
Strausberg R.;
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO73791; AA473791.1; -.
Interpro; IPR003599; IG.
Interpro; IPR003599; IG.
Interpro; IPR003596; IG.
Interpro; IPR0047; IG.
Interpro; IPR0047; IG.
IG; 2.
INTERPROSON IG.
IG; 2.
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IG; 3.
INTERPROSON IG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SECUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;
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Local Similarity 80.7 nes 92, Conservative
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SEQUENCE FROM N.A.
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Best Local S
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Q6PIH7
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Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow N.F., Carninci P., Frange C.,
A. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
N. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., García A.W., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Johes S.J., Marra M.J.,
Johes S.J., Marra M.J.,
Johes S.J., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                         MEDLINE-98375893; PubMed-9712075; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetyJglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.6%; Score 468.5; DB 2; Length 107; 84.8%; Pred. No. 4.6e-39; tive 5; Mismatches 7; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 236 AA
                                                                                                                        antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
                                                                                                                                                                                                                                                                 PIR; S16840; S16840.
PIR; S31977; S31977.
PIR; S34083; S34083.
PIR; S34086; S34083.
HNSP; PO1607; IBWW.
INTERPOY; IRRO07110; Ig-like.
INTERPOY; IRRO03596; Ig_v.
SWART; SWO0406; IGv; I.
                                                                                                                                                                                     U96396; AAB68785.1; -
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Matches 95, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
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Homo sapiens (Human).
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SEQUENCE
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EMBL; 1
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Richards R.D., Feingold B.A., Grouse L.H., Oberged J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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A Strausberg R.;
L Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
E EMBL; EC073775; AAH7375.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003006; Ig.HHC.
R InterPro; IPR003006; Ig.HHC.
R InterPro; IPR003006; Ig.V.
R Emp. PF07654; Cl.set; l.
R Pfam; PF07654; Cl.set; l.
DR SWART; SW00407; IG; 2.
DR SWART; SW00406; IG; 2.
SWART; SW00406; IG; 2.
DR SWART; SW00406; IG; 2.
SR SWART; SW00406; IG; 2.
DR SWART; SW00406; IG; 2.
SR SWART; SW00406; IG; 2.
SR SWART; SW00406; IG; 2.
SR SWART; SW00406; IG; 3.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A, 99:16899-16903(2002)
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Strausberg R.;

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108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
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ID KV1W HUMAN
AC P04431;
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P01597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin I chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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3D-structure; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity-determining-3. Framework 4. By similarity.
                                                                                                                                                                                                                                                                                                                             Length 236;
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Framework-2.
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         EMBL, BC034141, AAR3141.1; -. BMBL, BC03416, AR2.

InterPro; IPR00359; Ig_c1.

InterPro; IPR00359; Ig_c1.

InterPro; IPR00359; Ig_v.

Pfam, PF07654; C1-8et, I.

SMART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS50835; IG_MHC; UNKNOWN_1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
                                                                                                                                                                                                                                                                                                                                                               11; Indels
(JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.0%; Score 465; DB 2; 82.5%; Pred. No. 2.5e-38; tive 5; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Rappa chain V-I region Hau.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA.
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.5<sup>3</sup>
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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The amino acid sequence of a human kappa light chain.";

Los acid sequence of a human kappa light chain.";

Los acid sequence of a human kappa light chain.";

Los acid sequence of a human kappa light chain.";

Los acid sequence of a human kappa light chain.";

Elect protein sequence of a human kappa light chain.";

Biochem. V. 123:945-958(1971).

First processor acid sequence of a human kappa light chain has the INV (3) marker.

Roy: 00:0005576; C:extracellular; NAS.

Roy: 00:000576; 
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                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                     4 ;
                                                                                                                                                                                                                                                                                                                                                                              61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR
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t; Pred. No. 8.2e-38;
10; Mismatches 10; Indels
    Length 108;
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                                                                                           7; Indels
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Match 77.9%; Score 464; DB 1; Local Similarity 81.2%; Pred. No. 1.3e-38; tes 91; Conservative 10; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Last sequence update)
, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=72053133; PubMed=5124396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
05-JUL-2004 (Rel. 44, Last ann
1g kappa chain V-I region DEE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-li
                                                                               MEDLINE=70201507; PubMed=5447531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 71.4%;
Conservative 1
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HSSP; P01607; 1BWW.
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Homo sapiens (Human)
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57
89
98 1
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108 AA;
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nes 80; Conserv
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NCBI_TaxID=9606;
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DISULFID
NON TER
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Matches
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SO THE FETT TENT OF THE SO THE
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                                                                                                                                                                                                                                                                MEDLINE-85014148; PubMed-6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the Kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.0%; Score 453; DB 1; Length 129; llarity 81.1%; Pred. No. 2e-37; Conservative 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14069 MW; F941FA07D4AFC2F9 CRC64;
                      13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Walker precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 Appa chain V-I region OU.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A01883; NAILVELLE HSSP; P01607; 1BWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
(Rel. 05, Created)
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                                                                                                         Homo sapiens (Human)
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tes 90; Conserv
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                                                                                                                                                                                         NCBI_TaxID=9606;
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SEQUENCE FROM N.A.

TISSUE-Skeletal Muscle;
TISSUE-Skeletal Muscle;
TISSUE-Skeletal Muscle;
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTZSPSSLSASVGBRVTITCRASZTI----SSYLBWYZZKPGKAPBLLIYAASBLHS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                              Science 169:56-59(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) mare.!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Framework-1.
Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%; Score 450; DB 1; Length 108; 71.4%; Pred. No. 3.3e-37; tive 19; Mismatches 9; Indels
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34 Complementarity-determining-
49 Framework-2.
56 Complementarity-determining-
88 Framework-3.
97 Complementarity-determining-
107 Framework-4.
88 By similarity.
88 By similarity.
88 By similarity.
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Last sequence update)
Last annotation update)
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
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KV1V HUMAN
P04430;
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., 'Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                         DIOMTOSPSSLSASVGDTVTITCRASQDI----SNYLAWFQQKPGKAPKSLIYGASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloghys. Struct. Mech. 1:139-146(1975).

-!- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REI.

-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scnwager F., stelgemann W., schramm H.J.;
"The structure determination of the variable portion of the Bence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=72189444; PubMed=5028201;
Schiechl H., Hilachmann N.;
"Rule of antibody structure. The primary structure of a monoclona:
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman B.E.,
Schwager P., Steigemann W., Schramm H.J.;
                                                                                                                         TISSUB-Skeletal Muscle;
TISSUB-Skeletal Muscle;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005332; AAH05332.1; -.
HSSP; P01834; 1HRZ.
InterPro; IPR001110; Ig-like.
InterPro; IPR001110; Ig-like.
InterPro; IPR003597; Ig-cl.
R InterPro; IPR003597; Ig-cl.
R Pfam; PP07654; Cl-set; I.
R PRM: SMART; SM0406; IG-set; I.
R PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
Q SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                      Score 446; DB 2; Length 23
Pred. No. 2e-36;
8; Mismatches 13; Indels
                                                                                                      ?roc. Nat1. Acad. Sci. U.S.A. 99:16899-16903(2002).
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[2]
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                       74.8%;
                                                                                                                                                                                                                                                                                                                                                                      78.1%;
                                                                                          cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 78.1:
nes 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein Au."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein Au).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV1B HUMAN
P01594;
                                                                                          and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones
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1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2; Dwnler F.B., O'Connor T.P., Benson M.D.; Polymorphism in a kappa I primary (AL) amyloid protein (BAN)."; Mol. Immunol. 23:73-78(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
PDB; 1JV5; X-ray, A=1-107.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005923; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PR00407; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 74.7%; Score 445; DB 1; Length 108; Similarity 79.5%; Pred. No. 1e-36; B9; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                      Complementarity-determining-3.
                                                                                                                                          Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                                             Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11939 MW; E8011187EE6F6FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
IJ kappa chain V-I region BAN.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA
                                                                                                                                                                                                                                  By similarity.
                                                                                                                                                                                             Framework-3.
                                                                                                                                                                                                                      Framework-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                               Immunoglobulin V region.
DOMAIN 1 23
                                                                                                                                           Best Local Similarity
Matches 89; Conserv
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Search completed: June 3, 2005, 09:16:13
Job time : 33.7497 secs
                                                                             KV1M HUMAN
P01605;
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SEQUENCE
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                                                                                                                                                                                                                                                              1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 60
                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVIITCRASQSI----SNYLNWYQQKPGKAPNLLIYAASSLQS 56
                                                                                                                                                                                                                                                                          1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                      61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Buthazoa, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.4%; Score 443.5; DB 2; Length 107; 79.5%; Pred. No. 1.5e-36; ative 8; Mismatches 10; Indels 5.
                                                                  Score 445; DB 1; Length 108;
Pred. No. 1e-36;
8; Mismatches 11; Indels
                                                                                                                    Complementarity-determining-1.
                                                                                                                                        Complementarity-determining-2.
                                                                                                                                                            Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                    11840 MW; CD3PD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; IBWW.
                                                                                                                                                                                                                                                                                                                                                                            107 AA
                                                                                                                                                                                By similarity
                                                                                                                                                   Framework-3.
                                                                                                          Framework-1
        HSSP; P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003855; P:immune response; NAS.
INTERPRO; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PR051TE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                      74.78;
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Matches 89; Conservative
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PIR; A01878; KIHUBN
                                                                                                                                                                                                     108 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete amino survived sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities."; Scand. J. Immunol. 5:677-684(1976).

-! AISCELLANGUS: The second and third hypervariable regions of this ohain are identical with those of the human POM V-III kappa chain, with which it shares certain idiotypic determinants.
-! AISCELLANGOUS: This chain was isolated from an IgM with anti-gamma globulin activity.
-! AO1871; KIHULY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMIQSPSSLSVSVGDRVTITCQASQNV----NAYLNWYQQKPGLAPKLLIYGASTREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQLIQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GVPSRFSGSGSGTDFTFIISSLQPEDIATYYCQQYNNWPPFFGGGTKVEVKR 108
                            GVPSRFSGSGSGTDFTLTISGLQAEDFATYYCQQSY-SALTFGPGTKVDIRR 107
61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Framework-1.
Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 443; DB 1; Length 108;
Pred. No. 1.6e-36;
8; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct protein sequencing; Immunoglobulin V region.

1 23 Framework-1.

DOMAIN 24 34 Complementarity-determ:
                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1G Kappa chain V-I region Lay.
Homo sapiens (Human)
                                                                                                                                                                    108 AA
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Best Local Similarity 78.6%;
Matches 88; Conservative
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                                                                                                                                                                 STANDARD;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	, using sw model	June 3, 2005, 08:29:47; Search time 37.3502 Seconds
Copyright	OM protein - protein search, using sw model	Run on: June 3, 200

(without alignments) 1180.467 Million cell updates/sec

US-10-791-619-8 596 1 DIQLTQSPSSLSASVGDRVT.....SHEDPYTFGQGTKVEIKRTV 114 Title: Perfect score: Sequence:

2105692 segs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:* geneseqp1980s:* Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:*geneseqp20000s:* geneseqp2001s:*

geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab76942 Variable	Adn07029 Anti-IqE	_	_	Aab47087 Anti-IgE	Aab76949 Full leng	Aab76951 Full leng	Aab76953 Variable	Aab76958 Variable	Adn07045 Anti-IgE	Adn07036 Anti-IgE	Adn07038 Anti-IgE	Adn07040 Anti-IgE	Aaw95653 Mus muscu	Aaw95660 Mus muscu	Aaw95662 Mus muscu	Aay50030 Human E27	Aab07472 Amino aci	Aab74211 E27 anti-	Abu62797 E27 anti-	Adf69597 Human ant	Adf29038 Anti-IgE	Aaw95668 Mus muscu	Aaw95667 Mus muscu	Aab76957 SFv fragm
OI	AAB76942	ADN07029	AAW95664	AAW95669	AAB47087	AAB76949	AAB76951	AAB76953 .	AAB76958	ADN07045	ADN07036	ADN07038	ADN07040	AAW95653	AAW95660	AAW95662	AAY50030	AAB07472	AAB74211	ABU62797	ADF69597	ADF29038	AAW95668	AAW95667	AAB76957
DB	4	œ	~	7	4	4	4	4	4	ω	œ	80	œ	~	~	N	~	٣	4	9	7	-	N	~	4
% Query Match Length DB	114	114	218	218	218	218	218	218	218	218	218	218	218	114	218	218	218	218	218	218	218	218	248	248	248
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.7	99.7	99.7	99.7	99.7	99.7	7.66	99.7	99.7	98.5	98.5	98.5
Score	596	596	296	296	296	296	296	296	969	296	296	969	296	594	594	594	594	594	594	594	594	594	587	587	587
Result No.	-	8	m	4	5	9	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aab76956 SFV fragm Adn07044 Anti-1gE Adn07043 Anti-1gE Aab76943 Variable Adn07030 Anti-1gE Adn07030 Anti-1gE Adn07031 Anti-1gE Aaw95655 Mus muscu Aaw95655 Mus muscu Aaw95658 Mus muscu Aaw95658 Mus muscu Aaw95658 Mus muscu Aaw95658 Mus muscu Aaw9669 Mus Anti-1gE Adn07034 Anti-1gE Adq90719 Anti-1gE Adq90719 Anti-1gE	Aar33312 Humanised Aaw95651 Mus muscu Aab76940 Variable Adn07027 Murine an
AAB76956 ADNO7044 ADNO7044 ADNO7043 AAB76943 AAN97030 AAN95655 AAN95655 AAN95655 AAN95658 AAN95658 AAN976944 ADNO7031 AAN95679 ADNO7034 ADNO7034 ADNO7034 ADNO7034	AAR33312 AAW95651 AAB76940 ADN07027
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 2 6 4 3 5 4 3

ALIGNMENTS

AAB76942 standard; protein; 114 AA. (first entry) 17-APR-2001 AAB76942; RESULT 1 AAB76942

Variable light chain sequence of e26 and e27 SEQ ID 8.

Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.

Synthetic.

US6172213-B1.

09-JAN-2001.

30-JUN-1998;

97US-0051554P. 02-JUL-1997;

98US-00109207.

(GETH) GENENTECH INC.

Lowman HB, Presta LG,

Lowe J;

Jardien PM,

WPI; 2001-122353/13.

New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity maturation with phage display

Disclosure; Fig 2; 87pp; English.

improved anti-IgE antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to somerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic, antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, utticaria and food allergies. The mutant antibodies produced by the above mentioned This invention relates to a nucleotide sequence encoding an antibody with

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               diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936-AAB76960 represent fragments of anti-Igs antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-Igs antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
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                                                                                                                                                                                                       1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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 acids may also be used as affinity purification agents and in
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                              61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                GVPSRFSGSGSGTDFTLTISSLQPEDFATYXCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder; therapy; attopic allergy; anaphylactic hypersensitivity; asthma; allergic rhintis; conjunctivitis; eczema; urticaria; food allergy; variable light chain domain; VL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-IgE antibody e26 and e27 variable light chain domain (VL)
                                                                                                                                          ; Score 596; DB 4; Length 114;
; Pred. No. 1.2e-35;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 8; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   ADN07029 standard; protein; 114 AA.
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/label= CDR-L2
93..100
/label= CDR-L3
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/label= CDR-L1
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98US-00109207.
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                                                                                                                                                            Best Local Similarity Love.
Matches 114; Conservative
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                                                                                                                  Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                               Query Match
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ADN07029
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88333333388
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The invention relates to therapeutic compositions comprising anti-IgB antibody or IgB binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgB-mediated disorders. The disorders include atopic allergy associated with

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable light Fab fragment, antibody; anti-IgE; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria; IgE.
                                                                                                                                                                                                             1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                                                              1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                  61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IGE antibody variable light chain domain (VL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus anti-1gE e26 & e27 variable light chain Fab fragment
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                                                                                                    Length 114;
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                                                                                                      100.0%; Score 596; DB 8;
100.0%; Pred. No. 1.2e-35;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                       AAW95664 standard; protein; 218
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                                                                                                   Query Match
Best Local Similarity 100.
Matches 114; Conservative
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                                                                     Sequence 114 AA;
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Light chain; heavy chain; anti-IgE antibody; E26; transfection; green fluorescent protein; GFP; promoter; expression.

11-JUL-2000; 2000WO-US018841.

#O200104306-A1

18-JAN-2001.

sapiens musculus

Ношо

Chimeric.

Anti-IgE antibody, E26, light chain.

(first entry)

11-SEP-2003 08-MAY-2001

AAB47087;

AAB47087 standard; protein; 218 AA

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Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
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                                                                                                                                                                                                                                                                                                             Variable light chain, IgE, antibody, anti-IgE, reduction, prevention, histamine; production, hypersenaitivity, allergen, anaphylaxis; atopic allergy, asthma, allergic rhinitis; conjunctivitis; hay fever; eczema, anaphylactic shock, urticaria; F(ab)'2 fragment.
Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2fragment.
                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                               GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV
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                                                                                                                                                                              AAW95669 standard; protein; 218 AA
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The sequences given in AAB47087-88 represent the light and heavy chains of the anti-1gE antibody, E26. These sequences were expressed by the construct of the invention, which comprises an amplifiable selectable gene, a green fluorescent protein gene (GFP), and a selected sequence encoding a desired product, which is operably linked to either the amplifiable selectable gene or to the GFP gene, and to a promoter. Constructs such as this, are useful for producing a desired product by introduction into a suitable eukaryotic cell, culturing the resultant eukaryotic cell under conditions so as to express the desired product, and recovering the desired product from the culture medium. The constructs are efficient for identifying and selecting for stable constructs are efficient for identifying and selecting for stable suitable for earlier and faster screening of transfected cells. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide construct for screening and obtaining cells expressing high levels of desired protein, comprises amplifiable selectable gene, fluorescent protein gene and sequence encoding desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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100.0%; Pred. No. 2.1e-35;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                               Krummen LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 13A; 75pp; English.
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
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AC AAB7
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AAB76949

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Gaps

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1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLWYQQKPGKAPKLLIYAASYLES

100.0%; Score 596; DB 2; Length 218; 100.0%; Pred. No. 2.1e-35; ive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 114; Conservative

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Query Match

GVPSRFSGSGSGTDFTLFISSLQPEDFATYYCQOSHEDPYTFGQGTKVEIKRTV 114

RESULT

Full length light chain sequence of e27 SEQ ID 17.

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Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                        New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                           Full length light chain sequence of e26 SEQ ID 15.
                                                                                                                                                                                                    Jardieu PM,
                                                                                                                                                                                                                                                                                        Claim 2; Fig 12; 87pp; English.
                                                                                                                                                                                                                                                                       maturation with phage display
                                                                                                                                             98US-00109207.
         (first entry)
                                                                                                                                                                                                    Lowman HB, Presta LG,
                                                                                                                                                                                 (GETH ) GENENTECH INC.
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                                                                                                       US6172213-B1
                                                                                                                                            30-JUN-1998;
          17-APR-2001
                                                                                                                          09-JAN-2001
                                                                                     Synthetic
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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgB antibody activity. The antibody has improved action due to a process comprising, a) identifying separtyl residues prone to isomerisation in unimproved anti-IgB (immunoglobulin B) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiathmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgB-mediated disorders couch as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in changes for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AABNF036. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgE antibodies

100.0%; Score 596; DB 4; Length 218; 100.0%; Pred. No. 2.1e-35; tive 0; Mismatches 0; Indels (Best Local Similarity 100. Matches 114; Conservative

1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES Gaps ô

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61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114

AAB76951 standard; protein; 218 AA. AAB76951; RESULT 7

17-APR-2001 (first entry)

improved anti-IgB antibody activity. The antibody has improved action due to a process comprising, a) identifying asparryl residues prone to shown a process comprising, a) identifying asparryl residues prone to substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological, dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The muteant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgB antibodies This invention relates to a nucleotide sequence encoding an antibody with Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy. New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity 1 DIQLIQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES Gaps 61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114 ö Length 218; 100.0%; Score 596; DB 4; 100.0%; Pred. No. 2.1e-35; tive 0; Mismatches 0; Lowe J; Jardien PM, AAB76953 standard; protein; 218 AA Claim 4; Fig 12; 87pp; English. maturation with phage display 98US-00109207 97US-0051554P 114; Conservative Lowman HB, Presta LG, (GETH) GENENTECH INC. WPI; 2001-122353/13 Local Similarity Sequence 218 AA; 30-JUN-1998; 02-JUL-1997; US6172213-B1 09-JAN-2001. Synthetic. AAB76953; Query Match Best Loca Matches RESULT 8 AAB76953 ZXXEXE EXEXXX 셤 8 ö 9 9

61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYCQQSHEDPYTFGQGTKVEIKRTV 114 Variable light chain Fab fragment of e26 and e27 SEQ ID 19. (first entry) 17-APR-2001

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antiinflammatory; Ig B; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.

New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity

maturation with phage display

Jardien PM,

Lowman HB, Presta LG, (GETH) GENENTECH INC

WPI; 2001-122353/13

98US-00109207. 97US-0051554P.

US6172213-B1

39-JAN-2001.

02-JUL-1997; 30-JUN-1998;

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Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig B; immunoglobulin B; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                  New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                                                                                                                  Lowe
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                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                  WPI; 2001-122353/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                           US6172213-B1
                                                                                             30-JUN-1998;
                                                                            09-JAN-2001
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Matches 114;
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                                           Synthetic
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improved anti-Interest of a nucreous sequence improved action due to a process comprising, a) identifying aspartyl residues prone to sequencisation in unimproved anti-IgE (immunoglobulin E) antibody **Intibody with substituting alternative residues to create candidate molecules, and of selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallargic; ophthalmological, dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivities, eczema, urticaria and nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antioned in specific cell, tissues or serum. Amino acid sequences AAB76936.

AAB7660 represent fragments of anti-IgE antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-1gs antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a nucleotide sequence encoding an antibody with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in specific cell, tissues or serum. Amino acid sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgE antibodies
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Anti-IgE antibody e26 and e27 variable light (VL) F(ab)' 2 fragment
61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                           GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder; therapy; atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
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New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                     New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                 The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL).
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98US-00109207.
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                                                                           Presta LG,
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 30-JUN-1998;
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30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL) F(ab)' 2
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                                                                                                                                                                                                                                                                                           Jardien PM,
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variable light chain; VL
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                                     Unidentified
                                                                           US6723833-B1
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                         The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allersy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL).
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                                                                                                                                                              Length 218;
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100.0%; Pred. No. 2.1e-35;
iive 0; Mismatches 0;
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SEQ ID NO 17; 89pp; English.
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                                                                                                                                     Sequence 218 AA;
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 Claim 1;
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The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eccema, utricaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL) Pab fragment.

Sequence 218 AA;

Claim 7; SEQ ID NO 19; 89pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
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                                                                                           1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
                                                                      1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES
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                                                                                                                                                                                                                                                                                                                                                                                                 Variable light chain; IgE; antibody; anti-IgE; reduction; prevention; histenmine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic thinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                       Gaps
                                                                                                                                       61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
                                                                                                                                                       GVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGGGTKVEIKRTV 114
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                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus anti-IgE e26 & e27 variable light chain.
   Score 596; DB 8;
Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 594; DB 2;
99.1%; Pred. No. 1.6e-35;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lowe J;
                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 89; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jardieu PM,
                                                                                                                                                                                                                                                             AAW95653 standard; protein; 114
                                    ő
 100.0%;
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                                                                                                                                                                                                                                                                                                                                (first entry)
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                                     114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-106057/09.
                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9901556-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1998;
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Query Match
Best Local S:
Matches 114
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RESULT 15

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The sequence is that of the full length light chain of e26. It was used as part of a method to improve the affinity of anti-1gE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, actor, allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                Light chain; IgE; antibody; anti-IgE; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                                                                                 Mus musculus anti-IgE e26 full length light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                   Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 94-95; 129pp; English.
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AAW95660 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                   98WO-US013410.
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                                                                  (first entry)
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                                                                08-JUN-1999
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                                  AAW95660;
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61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYXCQQSHEDPYTFGQGTKVEIKRTV 114

Search completed: June 3, 2005, 09:09:07 Job time : 38.3502 secs

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5.1.6	Compugen
ersion	- 2005
GenCore v	(c) 1993
	Copyright

OM protein - protein search, using sw model

June Run on:

3, 2005, 08:53:28 ; Search time 7.09576 Seconds (without alignments) 1545.812 Million cell updates/sec

score: Title: Perfect

US-10-791-619-11 623 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVWGQG 114 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:* Database

pir1:*

3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	heavy chain V		heavy chain	Ig heavy chain V r	Ig heavy chain - h	Ig variable region		Ig heavy chain V r	Ig heavy chain V r	heavy chain V	heavy	heavy chain -	heavy chain -	heavy	heavy	heavy	heavy	heavy	heavy chain V	heavy	heavy chain V		heavy chain V	heavy	heavy	heavy chain	heavy cha	heavy cha	Ig heavy chain - h
SUMMARIES	ID		S70442	_	S31666	S31113	137780	E36005	S48797	S31669	830531	S36259	S31107	S31117	S19666	G36005	S31598	S31686	S38489	S31701	S26794	S20782	S36280	S31587	S31108	S05271	8	S23624	831603	Ξ
	08	7	~	~	7	~	N	0	~	~	~	~	~	~	7	~	7	~	~	~	~	7	~	~	N	~	0	2	~	N
	Length	140	140	123	138	121	147	122	128	141	125	117	119	122	121	121	135	140	127	137	123	124	114	136	119	160	119	143	132	116
d	Query	67.3	67.2	67.1	8.99	66.3	66.1	65.7	65.7	65.7	65.5	65.3	65.3	64.9	64.8	64.8	64.8	64.8	64.7	64.4	64.4	64.3	64.1	64.1	64.0	64.0	63.9	63.9	63.7	63.6
	Score	4	418.5	418	416	413	$\overline{}$	409.5	8	409.5	408	407	407	404.5	404	404	404	404	403	401.5	401	0	399.5	9	399	399	398	398	397	396.5
	Result No.	-	7	٣	4	2	9	7	80	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain V-I Ig heavy chain V r Ig variable region	Ig heavy chain - h Ig heavy chain v r Ig heavy chain v r	Ig heavy chain V r Ig heavy chain - h Ig heavy chain V r	Ig heavy chain V r anti-tetanus toxin Ig heavy chain V r	
M3HUBW S31601 I37781	S31116 S48798 S31674	C36005 I55673 S31699	S46390 PC2398 F36005	S31679 M3HUAM S26790 S78486
100	000	0 00 00	01 01 00	0 11 10 10
120 130	118 120 139	119 121 134	114 122 119	134 122 128 117
63.6 63.6 63.6	63.5	63.4 63.4 63.4	63.3 63.3	63.2 63.2 63.1
396 396	395.5 395.5 395.5	395 395 395	394.5 394.5 394	394 393.5 393.5
30	3 3 3 3 1 5 4 5 3	36 37 38	39 41 41	4 4 4 4 2 6 4 2 5 4 5

ALIGNMENTS

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Using the peary chain V region - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Sacession: S31588
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the fargerence number: S31588
A; Reference number: S31588
A; Reference preliminary
A; Molecule type: mRNA
A; Residues: 1-140 <CUI>A; Cross-references: EMBL: Z14200; NID:g30957; PIDN: CAA78569.1; PID:g30958
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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Best Local S:
Matches 82
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RESULT 2 S70442

Ig heavy chain precursor V region (mu) - human (fragment) C;Species: Homo sapiens (man) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: 1904 kappas/lambda EBV human B cell clone: an early step of differentiation of fet A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Reference number: compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPROT:QBWUKI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 418.5; DB 2; Length 140; Best Local Similarity, 72.2%; Pred. No. 2.7e-30;

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C;Species: Howo sapiens (man)
C;Dacte: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31113
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Bur. J. Immunol. 22, 247-2511, 1999
Rur. J. Immunol. 22, 247-2511, 1999
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig variable region (VDJ) (clone T20-11) - human (fragment)

[c;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C;Accession: 137780; S25474

R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X62962
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSS-YAMSWVRQAPGKGLEWVSAISGSGGSTY 59
                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: S11113
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
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   79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAR--TGYWYFDLWGRG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579 C;Superfamily: immunoglobulin V region; immunoglobulin homology <I,MM>
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A; Residues: 1-147 <RES>
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R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A; Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S31666
C;Accession: S31666
C;Cuisonier, A.W.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Superfamily: immunoglobilin V region; immunoglobilin homology C;Keywords: heterotetramer; immunoglobilin C;Keywords: heterotetramer; immunoglobilin homology <IMM>
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                                                                  29
                                                                                           20 QVQLVESGGGVVQPGGSLRLSCAASGFTF-SNYGMHWVRQAPGKGLEWVAFIRYDGSNKY 78
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A, Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Species: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                                                               EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
      3; Gaps
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   20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.1%; Score 418; DB 2; 71.8%; Pred. No. 2.7e-30;
   9; Mismatches
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Ig heavy chain V region - human (fragment)
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   Conservative
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Best Local Similarity
Matches 84; Conserv
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A;Residues: 1-138 <CUI>
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83;
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 53169
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the & A;Reference number: S31585
A;Accession: S31669
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S36259
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Ttle: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 EVQLVESGGGLVKPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKGLEWVSSISSSSXIY 78
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Cispecies: Misseriete
Cispecies: Misseriete
Airolantied to the EMBL Data Library, October 1992
Airolantied to the EMBL Data Library, October 1992
Airolanties: Sabisa
Airolanties preliminary
Airolanties preliminary
Airolanties the MRA
Airolanties: Homo and Airolanties
Cispecies: UNIPROT: QUIL91; EMBL: Z18317
Cispecies: Inmunoglobulin V region; immunoglobulin homology
Circycords: heterotetramer; immunoglobulin
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69.2%; Pred. No. 2.1e-29;
ive 11; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
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82;
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Best Local S:
Matches 82
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R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: B36005
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A; Residues: 1-128 «MAIS.
A; Cross-references: EMBL: 246379; NID: 9587147; PIDN: CRA86512.1; PID: 91340168
A; Cross-references: EMBL: 246379; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
Mol. Biol. 227, 776-798, 1992
A; Fitle: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Reference number: $26885; MUID: 93021117; PMID: 1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMSL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.7%; Score 409.5; DB 2; Length 122; 70.1%; Pred. No. 1.5e-29;
                                                                                                                                                                                                                                                                                                                          A,Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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67.2%; Pred. No. 1.6e-29;
iive 15; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 1.5e-29; 11; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                  A;Cross-references: GB:M34030
C;Genetics:
                                                                                                                                                                                                                                                                                                 A; Gene: GDB: IGH@; IGHDY1
                                                                                                                                                   A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-122 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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A; Residues: 1-98 <TOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 QG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S26893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: S48797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
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Best Local &
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Length 122;

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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #text_change 20-Jun-2000
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phane A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., Hw.; Wang, J.Y.
R;Schroeder Jr., Hw.; Wang, J.Y.
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene & A;Reference number: A36005; MUID:90349571; PMID:2117273
                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK- 59
                                                                                                                                                                                                                          A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heteroterramer; immunoglobulin PC;Reywords: heteroterramer; immunoglobulin P;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
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                                                                                                                                                                                                                                                                                                                                                     60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDFFAPPNWSHFDYWGG 115
                                                                                                                                                                                                                                                                                                                    60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHW-HFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.8%; Score 404; DB 2; Length 121; Best Local Similarity 68.7%; Pred. No. 4.6e-29; Matches 79; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB:1GH0; IGHDY1
A; Cross-references: GDB:118731; OMIM:146910
A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heteroterramer; immunoglobulin P;15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                          22; Indels
                                                     DB 2;
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                                                        Score 404.5; DB 2
Pred. No. 4.1e-29;
                                                                                                                       9; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region (VH3DJH4) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (M74) - human
                                                        ch
1 Similarity 70.7%;
82; Conservative
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Matches 81; Conservative
                                                           Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-121 < MAR>
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S19666
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CyAccession: S31107
Rikaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Biraaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 241-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31107
A;Accession: S31107
A;Accession: Translation not shown
A;Molecule type: mRNA>
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A;Rolecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMED:X62967
A;Cross-references: EMED:X62967
A;Notes the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin Nomology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFG----HWHFAVWGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                                                                                       A;Cross-references: EMBL:Z18850; NID:g33123; PIDN:CAA79302.1; PID:g939902 Cs.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                         Length 117;
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                                                                                                                                                                                                                                                                                                                                                  21; Indels
                          A;Status: preliminary, nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-117 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 65.3%; Score 407; DB 2;
1 Similarity 70.9%; Pred. No. 2.4e-29;
83; Conservative 12; Mismatches 14,
                                                                                                                                                                                                                                                                                      65.3%; Score 407; DB 2; 68.6%; Pred. No. 2.4e-29;
                                                                                                                                                                                                                                                                                   Query Match 65.3%; Score 407; DB Best Local Similarity 68.6%; Pred. No. 2.4e-Matches 81; Conservative 10; Mismatches
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Best Local Similarity
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   A; Accession: S36259
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US-10-791-619-11 623 1 EVQLVESGGGLVQPGGSLRL......XCARGSHYFGHWHFAVWGQG 114 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	sapien		sapien	sapien		sapien		sapien											mus musculu	carassius a									musculu		
tion	homod	homod	homo	homod	homo	рошо	homo	рошо	рошо	homod	рошо	homo	рошо	homod	рошо	homo	homo	homo	mus 1	cara	рошо	homo	homo	homo	homod	homod	рошо	homod	mus	рошо	Ę
Description	Q6pja4	09u190	Q6in78	Q6pi81	Q9u172	P01766	Q8wuk1	Q65zc9	Q6n089	P01768	Q9u191	Q6mzv7	Q6gmy2	69960	Q6mzg6	Q9u193	Q9u171	Oemzne Oemzne	P01793	P19181	Q8wu38	Q9y509	P01764	Q6gmx2	Q96k68	Q9hcc1	QBncl6	P01767	P01791	Q8n5k4	077100
						IAN				IAN									ISE	AU			IAN					IAN	ISE		TA KI
ID OI	Q6PJA4	Q9UL90	Q61N78	Q6P181	Q9UL72	HV3E HUMAN	QBWUK1	Q652C9	06N089	HV3G HUMAN	Q9UL91	CVZM3Q	O6GMY2	Q96BB9	90ZW90	09UL93	Q9UL71	Q6MZU6	HV24 MOUSE	HV05_CARAU	Q8WU38	Q9Y509	HV3C HUMAN	Q6GMX2	Q96K68	Q9HCC1	OBNCF6	HV3F HUMAN	HV22_MOUSE	Q8N5K4	MANATA TOTAL
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% Query Match Length DB	470	113	466	478	118	120	613	240	472	122	118	473	909	597	475	116	121	464	123	116	573	147	117	493	494	112	493	115	123	499	9
% Query Match	66.3	65.5	64.0	63.9	63.8	63.6	63.3	63.2	63.2	63.2	63.0	62.8	62.8	62.8	62.5	62.4	62.4	62.4	61.8	61.7	61.6	61.4	61.3	61.2	61.1	9.09	60.5	60.09	60.0	60.0	0
Score	413	408	399	398	397.5	396	394.5	394	394	393.5	392.5	391.5	391.5	391	389.5	389	389	389	385	384.5	383.5	382.5	382	381	380.5	377.5	377	374	374	374	273
Result No.	-	8	ო	4	ς.	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	2.1

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Q80ZI7 HV3J HUMAN	HV20 MOUSE	Q6ZVX0	Q725W1	HV3B HUMAN	HV21 MOUSE	Q99KA4	HV18 MOUSE	HV23 MOUSE	HV19_MOUSE	HV46 MOUSE	HV30_MOUSE
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487	122	479	470	114	122	487	123	123	123	137	113
59.6	59.3	59.1	58.9	58.8	58.8	58.8	58.6	58.6	58.4	58.4	58.3
371 370	369.5	368.5	367	366.5	366.5	366.5	365	365	364	364	363
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ALIGNMENTS

RESULT 1

Depund of Depund PRELIMINARY; PRT; 470 AA. Depund of CARFAGLER 127, Created) DT 05-JUL-2004 (TrEMGLER1. 27, Last sequence update) DE MOON SEQUENCE ROAD AND AND AND AND AND AND AND AND AND A

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TISSUEPE FROM N.A.

TISSUE-PETIPHERAL Nervous System;

TISSUE-PETIPHERAL Nervous System;

REDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RASTAURDEPET R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;

RAJUREL R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

Altschul S.F.; Zeeberg B. Buetow K.H.; Schaefer C.F.; Bhat N.K.;

HOPKINS R.F.; Jozdan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;

LA Brownstein M.S.; Dozdan H.; Moore T.; Marmary J.; Hsieh P.;

Rapleton M.; Soares M.B.; Bonaldo M.F.; Carninci P.; Prange C.;

Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Millahy S.J.;

Roask S.A.; McZwan P.J.; McKernan K.J.; Malek J.A.; Gunarane P.H.;

Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

Nilalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Rahey J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.;

Miting M.; Madan A.; Young A.C.; Shevchenko Y.; Boutfard G.G.;

Makesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

M. Jones S.J.; Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Homo sapiens (Human).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
     NCBI_TaxID=9606;
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                                                                                                                                                                           1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                                                      79 YVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDW-FDPWGQG 133
                                                                                                                                                                                                                                                                              61 N-PSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCAR-GSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.5%; Score 408; DB 2; Length 113;
Best Local Similarity 70.4%; Pred. No. 8.2e-34;
Matches 81; Conservative 10; Mismatches 14; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK-
                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLNY------WGQG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                        Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin-reactive immunoglobulin heavy chain variable region
                                                                      cch 66.3%; Score 413; DB 2; Length 47 al Similarity 72.4%; Pred. No. 1.2e-33; B4; Conservative 11; Mismatches 17; Indels
Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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BIR; STR486; ST8486.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR0075596; Ig-v.
SMART; SM00406; IG-v; I-.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Name=IGHG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment)
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NON_TER
SEQUENCE
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Q9UL90
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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGNYVV---PAAPWGQG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                 20; Indels
                                                                        TISSUE=Peripheral Nervous System;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 399; DB 2;
%; Pred. No. 3.2e-32;
11; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               69.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6P181;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                 EMBL; BC072419; AAH72419.1;
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Conservative
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TISSUE=Primary B-Cells;
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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYS-GETK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNY-MNWYRQAPGKGLESV-SVTYSGGSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the VH region of the IgM paraprotein.";
Immunochemistry 13:995-999(1976).
-!- MISCELLANEOUS: This chain was obtained from IgM isolated from the serum of a patient with malignant lymphoma of the Waldenstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 YADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAPYYCARDR--FGEFLFDYWGQG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
                                                                                                                                 'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%; Score 397.5; DB 2; Length 118; 72.2%; Pred. No. 1e-32; ive 9; Mismatches 18; Indels 5;
                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%; Score 396; DB 1; Length 12
65.0%; Pred. No. 1.5e-32;
ive 12; Mismatches 17; Indels
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HSSP; P01783; IIGC.
GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0006955; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00715; Ig-V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B4D1A5944B2D5CCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct protein sequencing; Immunoglobulin V region. DOMAIN
                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AP035042; AAD56278.1; -.
PIR; S21205; S21205.
HSSP; P01783; 11GC.
InterPro; IPR0017110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
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118 AA; 12872 MW;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 72.2
nes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 80; Conserv
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV3E HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
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                                                                                                                                                                           Eetus.";
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   셤
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                        Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Nausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Romatein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan K.J., Malek J.A., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Schmutz J., Myers R.W., Butterfield Y.S.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 EVÓLVESGGGLVOPGGSLRLSCAASGFTFSS-YMMSWVRQAPGKGLEWVANIKQDGSEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.9%; Score 398; DB 2; Length 478;
65.3%; Pred. No. 4.2e-32;
ive 15; Mismatches 16; Indels 12;
MEDLINE=22388257; Pubmed=1247.7932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Straubberg R.; | Straubberg R.; | Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. | Bubmitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. | Bubmitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. | EMSP; | PO1861; | LADO. | InterPro; | IPR003599; | Ig. | InterPro; | IPR003599; | Ig. | InterPro; | IPR003599; | Ig. | InterPro; | IPR003596; | Ig. | 
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Q9UL72
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28

Gaps

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14;

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613 AA; 67295 MW; 60C7F5950671E315 CRC64;
  SQ SEQUENCE
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                                                                                            Matches
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B.B., Branen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

B Altschun M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Stapleton M., Juddin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                              60 ADSVKGRPTISRNDSKNTLYLANMNSLRAEDTAVYYCARSPVSLVDGWLYYYYG---SVW 115
                                                                                                                  61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGS-----HYFGHWHFAVW 111
                        9
                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGFTF-SYYNMWWRQVTGKGLEWVSAIGTAGDQYY 59
                        EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Primary B-Cells;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                      613 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC020240; AAH20240.1;
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Pfam; PF07654; C1-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PH1643; PH1643.
PH1645; PH1645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PH1646; PH1646
PL0098; PL0098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                 112 GQG 114
                                                                                                                                                                                                                                                                116 GQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; F36005; PIR; PH1642; PIR; PH1642; PIR; PH1643; PIR; PH1645; PIR; PL0120; PIR; PL0120; PIR; S311119; PIR; S311119; PIR; S311119; PIR; S311119; PIR; S311119; PIR; S31119; PIR; S3119; PIR; S31119; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHM protein.
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60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH-----FAVWGQG 114
                                                                                                                                                 20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVISYDGSNKY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETK- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVISYDGSNKY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAV--WGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-----DWGDSLDPWGKG 110
                                                                                                                   1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITSGYSWNWIROAPGKGLEWVASIKYSGETK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th 63.2%; Score 394; DB 2; Length 240; Similarity 68.4%; Pred. No. 5e-32; 80; Conservative 11; Mismatches 16; Indels 10; Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Wasaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                           13;
  DB 2; Length 613;
; Score 394.5; DB 2; Length 6; Pred. No. 1.3e-31; 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kontermann R.E., Wing M.G., Winter G.,
"Complement recruitment using bispecific diabodies.";
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631 (1997).
EMBL; VI3056, CAA73499.1;
InterPro; IPR00110; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.v.
Pfam; PF00047; ig; 2.
SWART; SW00406; IG; 2.
SWART; SW00406; IGv; 2.
EMART; PF001RF; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G6N089 PRELIMINARY; PRT; 472 AA.
G6N089;
05-ULL-2004 (TrEMBLrel. 27, Created)
05-ULL-2004 (TrEMBLrel. 27, Last sequence update)
05-ULL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein DKFZp686P15220.
Name=DKFZp686F15220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C1q/7;
MEDLINE=97362799; PubMed=9219263;
  63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single-chain Fv (Fragment)
                                                           80; Conservative
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  Query Match
Best Local Similarity
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122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
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SEQUENCE
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Q6MZV7
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                                                                                                                                                                                                                                                                                                                                              20 EVQLVESGGGLVQPGRSLRLSCAASGFTF-DDYAMHWVRQAPGKGLEWVSGISWNSGSIA 78
                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKY-SGETK 59
                                                                                                                                                                                                                                                                                                                                                                                            60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR--GSHYFGHWHFAVWGQG 114
                     TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
The German B., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640627; CAE45781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lehman D.W., Putnam F.W.;
Lehman D.W., Putnam F.W.;

"Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

-i. MISCELLANBOUS: This mu chain was isolated from the plasma of
                                                                                                                                                                                                                                                                                Query Match 63.2%; Score 394; DB 2; Length 472; Best Local Similarity 66.7%; Pred. No. 1.1e-31; Matches 78; Conservative 14; Mismatches 21; Indels
                                                                                         HSSP; P01861; 1ADO.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003006; Ig. HG.
InterPro; IPR00356; Ig. HG.
InterPro; IPR00356; Ig. HG.
InterPro; IPR003596; Ig. HG.
InterPro; IPR00409; IG. 2.
SWART; SW00409; IG. 2.
SWART; SW00406; IGV; 1.
ROSITE; PSC0835; IG. LIKE; 4.
RPOSITE; PSC0835; IG. LIKE; 4.
Hypothetical protein.
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient with macroglobulinemia.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02051; M3HUAM.
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SMART; SMO406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.

Price protein sequencing; Immunoglobulin V region;

Pyrrolidone carboxylic acid. Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 AA
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
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              SEQUENCE FROM N.A.
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NON TER
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                                                                                                                                                                                                                                                                                1 QVELVVESGGGVVZPGRSLRLSCAASGFTF-SNYAMHWVRQPPGKGLEWVAVISYBGBBKY
                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NP-SVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQG 114
                                                                                                                   3; Gaps
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last annotation update)
16-JUL-2004 (TrEMBLrel. 27, Last annotation update)
17-JUL-2004 (TrEMBLrel. 27, Last annotation update)
17-JUL-2004 (TrEMBLRel. 27, Last annotation update)
17-JUL-2004 (TrEMBLRel. 27, Last annotate)
17-JUL-2004 (TrEMBLRel
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2
     DB 1; Length 122;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
Query Match 63.2%; Score 393.5; DB 1; Length Best Local Similarity 65.5%; Pred. No. 2.7e-32; Matches 76; Conservative 15; Mismatches 22; Indels
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EMBL, AR035023, AAD56259.1; -. PIR, S21205; PA0875.
PIR, S21205; S31205.
PIR, S30531; S30531.
HSSP, P01793; 11GC.
INCEPPO; IPR007110; Ig-like.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELAUSEER R.D., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,

M. Klausner R.D., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B. Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B. Diatchenko L., Morguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S. Worlery K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

M. Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

M. Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

M. Haltesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Jones S.J., Marra M.A.,

"M. Jones S.J., Marra M.J.,

"M. Jones 
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                                                                                                                                                                                                                  Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640853; CAE45920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                 HSSP, DO1861, 
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                      The German Human cDNA Consortium;
                                                                                                                                                   intestine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                       SEQUENCE FROM N.A.
TISSUE=Human small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O6GMY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
Q6GMY2
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TISSUE=Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=288 R.L., Grandler G.M., Schaefer C.F., Bhat N.K., Antechnis C.M., March N.K., March M., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Williadon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mriting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Marcia M., M., Marcia M., Morth M., Marcia M., Schalska U., Smailus D.E., Schnerch A., Schein J.E., Marcia M., Marcia M., Marcia M., Schein J.E., Schnerch A., Schein J.E., Marcia M., Marcia M., Marcia M., Shalska U., Smailus D.E., Schnerch A., Schein J.E., Marcia M., Marcia M., Marcia M., Schein J.E., Schnerch A., Schein J.E., Marcia M., Marcia M., Marcia M., Schein J.E., Schnerch A., Schein J.E., Marcia M., Marcia M., Marcia M., Sachein J.E., Schnerch A., Schein J.E., Marcia M., Marcia M., Marcia M., Sachein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schlerch A., Schein J.E., Schein J.E., Schlerch A., Schein J.E., Schlerch A., Schein J.E., Schlerch A., Schein J.E., Schlerch A., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGE-TK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 606;
A Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079758; AM47378.1; -.
InterPro; IPR00359; IG.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR0047; Ig. 4.
InterPro; IPR0047; Ig. 4.
InterPro; IPR0047; Ig. 4.
InterPro; IPR0047; Ig. 4.
InterPro; IPR00406; IG; Ig.
InterPro; IRR SMOA406; IG; IG.
InterPro; IRR SMOA406; IG; IG.
INTERPROSITE; PS00835; IG. LIKE; S.
INTERPROSITE; PS00835; IG. LIKE; S.
INTERPROSITE; PS00835; IG. LIKE; S.
INTERPROSITE; PS00839; IG. MIC; UNKNOWN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 AA; 66184 MW; B6B38B51114E4C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.8%; Score 391.5;
Local Similarity 62.5%; Pred. No. 2.5e
es 80; Conservative 13; Mismatches
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 HFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 GMDVWGQG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYS-GETK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCA---RGSHYFGHW-HFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Human esophagus tumor;
The German Human cDNA Consortium;
Lauber J., Bahr A., Newes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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Mammalia, Euthazia, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
9
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                                                                                                                                                           | Tisbusberg R.; | Strausberg R.; | Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. R EMBL; BC015760; AAH15760.1; -. | PRBL; S05271. | S05271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.8%; Score 391; DB 2; Length 597; Best Local Similarity 68.9%; Pred. No. 2.8e-31; Matches 82; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640947; CAE45972.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 475 AA; 52043 MW; B7BAB255A26F4B8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686G11190.
Name=DKFZp686G11190;
and mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SMART; SM00407; IGcl; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01861; JALO.
InterPro; IPR003599; IG.
InterPro; IPR003597; IG-11ke.
InterPro; IPR003597; IG-C1.
InterPro; IPR003506; IG-MHC.
InterPro; IPR003596; IG-V.
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                                                                                                          SEQUENCE FROM N.A.
[ISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Q6MZQ6
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Gaps

Conservative

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79 YADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRG 138
                                                                                                                60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYF----GHWHFAVWGOG 114
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSG-ETK 59
                               20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRN-YAMNWYRQAPGKGLEWVSGISSSGVNTY 78
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Search completed: June 3, 2005, 09:16:14 Job time: 33.7497 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

3, 2005, 08:53:28 ; Search time 7.09576 Seconds (without alignments) 1545.812 Million cell updates/sec June Run on:

US-10-791-619-12 625 1 EVQLVESGGGLVQPGGSLRL......YCARGSHYFGHWHFAVWGQG 114 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heavy chain	heavy		heavy	heavy			heavy		-			heavy chain		heavy	heavy			heavy	heavy		heavy	heavy	heavy	heavy		heavy	heavy cha	
SUMMARIES	ΩI	7044	S31588	S31114	831666	E36005	S48797	831113	831117	831669	137780	S19666	G36005	836259	S30531	S31107	831701	S31598	S31686	S38489	S31603	S26794	831601	831116	S31674	S46390	831108	F36005	31	805271
	DB		7	N	N	N	N	N	N	7	7	~	~	N	~	~	N	~	~	~	~	7	7	~	~	7	N	N	~	7
	Length	14	140	123	138	122	128	121	122	141	147	121	121	117	125	119	137	135	140	127	132	123	130	118	139	н	119	н	134	9
de	Query	67.3			66.7	99	66.5	٠,	65.7	65.7	65.7	9.59	65.6	65.4	65.4	65.3	65.2	65.0	64.8	64.6	64.5	64.3	64.3	64.2	•	64.1		64.0		64.0
	Score	20.5	420	419	417	415.5	'n.	Н	410.5	410.5	410.5	410	410	409	409	408	407.5	406	405	404	403	402	402	401.5	401.5	400.5	400	400	400	400
	Result No.		7	e	4	S	9	7	80	O	10	11	12	13	14		16	17		19		21	22	23		25		27	28	

Ig heavy chain - h	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	anti-tetanus toxin	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h	Ig heavy chain (su	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h
S31110	S20782	D36005	PL0098	S23624	S36280	S31587	PC2398	S36270	S48798	C36005	155673	S31104	831699	846391	S38493
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116	124	119	130	143	114	136	122	117	120	119	121	121	134	114	123
													_	_	٥,
63.9	63.9	63.8	63.8	63.8	63.8	63.8	63.6	63.5	63.4	63.4	63.4	63.4	63.4	63.	63.2
	399.5 63.9		_				_								_

ALIGNMENTS

RESULT 1 S70442	
Ig heavy	Ig heavy chain precursor V region (mu) - human (fragment)
C; Specie	C; Species: Homo sapiens (man)
C,Date:	C.bate: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C, Access	C:ACCEBELOI: S/U442 D:Cristist N N : Dimons B : Dougstell N : Formelle C
Mol. Imm	Kichibiniti, A.M.; Kamouda, K.; Kougereau, M.; Johnete, C. MMOl. Immunol. 29, 1363-1373, 1992
A; Title:	A; Title: IgM kappa/lambda BbV human B cell clone: an early step of differentiation of
A, Refere	A;Reference number: S70442; MUID:93024508; PMID:1383695
A ACCESS	AfficeSELUL: 97 Units Annually with Annualtical translation
A: Molecu	Afjectus not Compared with conceptual transferior A:Molecule type: mRNA
A:Residu	A; Residues: 1-140 < CUI>
A;Cross-:	A;Cross-references: UNIPROT:Q8WUK1
C;Superf	C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117	F;34-117/Domain: immunoglobulin homology <imm></imm>
Query Match	Query Match 67.3%; Score 420.5; DB 2; Length 140;
Matches	
ò	OPGGSLRLSCAVSGYSITSGYS
qq	20 QVQLVESGGGVVQPGGSLRLSCAASGFTF-SNYGMHWVRQAPGKGLEWVAFIRYDGSNKY 78
δ	60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
QQ	79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-DHIVGATYFDYWGQG 132

RESULT 2
\$31588
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: \$31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Reference number: \$31588
A;Reference number: \$31588
A;Reference number: \$31588
A;Reference rest EMBL: 214200, NID:930957; PIDN:CAA78569.1; PID:930958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <1MM>
F;34-117/Domain: immunoglobulin homology <1MM>

Length 140; Score 420; DB 2; Pred. No. 6.7e-30; 67.2%; Query Match Best Local Similarity ~

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Ig heavy chain V region (M72) - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (M72) - human (M72) - human (M72) - human (M72) - human (M72) (M72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues; 1-128 <a href="Mailto:AMB-1">AMB A; Residues; 1-128 <a href="Mailto:AMB-1">A; Residues; 1-128 <a href="Mailto:AMB-1">A; Residues; 1-128 <a href="Mailto:AMB-1">A; Cross = ***-references = ***-references = ***-references = ***-references = ***-references = ***-reference = ***-referen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: 848797; 826893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Rsubmitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVIWYDGSNKY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YAMFWVRQAPGKGLEWVAVISYDGSNKY 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFA--VWGQG 114
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79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAR--TGYWYFDLWGRG 131
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A;Residues: 1-98 «TOM»
A;Cross-references: EMBL:Z12350; NID:g32922; PIDN:CAA78220.1; PID:g32923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:IGH0; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Genetics:
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31666
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                                                                   EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIT-YDGSTN
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18; Indels
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Pred. No. 7.2e-30;
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13; Mismatches
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Best Local Similarity 71.8%
Matches 84; Conservative
Conservative
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A;Residues: 1-123 <RAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain - human
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Gaps

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Indels

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Ig variable region (VDJ) (clone T20-11) - human (fragment)

Ig variable region (VDJ) (clone T20-11) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C;Accession: 137780; S25474

R;Demaison, C; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by hts. R;Reference number: A36876; MUID:94119917; PMID:8290556
                                                                                      $31669

glacey chain V region - human (fragment)

Cjacesies: Homo sapiens (man)

Cjacesies: Homo sapiens (man)

Cjacession: S1469

R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
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g heavy chain V region (VH3DJH4) - human
G;gheavy chain V region (WH3DJH4) - human
G;Species: Home sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:214212; NID:g30959; PIDN:CAA78581.1; PID:g30960 (S.byperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin Pi34-117/Domain: immunoglobulin homology <INM>
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70.7%; Pred. No. 4.6e-29;
ive 13; Mismatches 18
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A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
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A;Molecule type: mRNA
A;Residues: 1-147 <RES>
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Best Local S:
Matches 82
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Date: 0.2 Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Ebr. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31117
A;Accession: S31117
                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S11113
R; Raaphorst, P.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A; Reference number: S31104; MUID:92111633; PMID:1730252
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A; Molecule type: mRNA
A; Residues: 1-122 - RAA>
A; Residues: 1-122 - RAA>
A; Cross-references: EMBL:X62967
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer: immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology F;IS-98/Domain: immunoglobulin homology r!IS-98/Domain: immunoglobulin homology 
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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIT-YDGSTN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision.26-May-1995 #text_change 17-Mar-1999
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71.6%;
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Matches 83; Conservative
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Best Local 3
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C, Accession: S31107
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, B.T. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme A; Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL Data Library, October 1991
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                                                                                                                                                                                                                                                                                               1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN- 59
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
                                                                                                                                                                                                                                                                                                                                                                                                                              60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFG----HWHFAVWGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 YADSVKGRFTISRDNSKYTLYLQMNSLRAEDTAVYYCVREDHVITTGRYHYYMDVWGK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S30531
R;Mariette, X.
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                   Gaps
   A;Cross-references: EMBL:Z18850; NID:g33123; PIDN:CAA79302.1; PID:g939902 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                   Score 409; DB 2; Length 117; Pred. No. 5.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9UL91; EMBL:218317
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 125
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A,Rote: the nucleotide sequence was submitted to the EMBL Data 1C; Superfamily: immunoglobulin V region; immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                               21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.4%; Score 409; DB 2; Best Local Similarity 69.2%; Pred. No. 5.5e-29; Matches 83; Conservative 12; Mismatches 17;
                                                                                                                                                   65.4%; Score 69.5%; Pred. No. 5.1e-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1992
A;Reference number: $30520
                                                                                                                                                             Query Match
Best Local Similarity 69.5<sup>3</sup>
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: S30531
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-125 < MAR>
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: 83629
Exigitiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: 836256; MUID:93178448; PMID:7679990
A;Accession: 83629
A;Accession: 83629
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
      면
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19666 A;Molecule type: mRNA A;Accession: S19666 A;Molecule type: mRNA A;Residues: 1-121 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hereroteramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
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                                                                                                                                                                                                                                                                                                                             Query Match 65.6%; Score 410; DB 2; Best Local Similarity 69.6%; Pred. No. 4.3e-29; Matches 80; Conservative 13; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.6%; Score 410; DB 2; ilarity 71.3%; Pred. No. 4.3e-29; Conservative 11; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Crose-references: UNIPROF:Q8WUK1; GB:M34031
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Query Match Best Local Similarity Matches 82; Conserv

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C;Genetics: A;Gene: GDB:IGH@; IGHDY1

Ig heavy chain V region (M74) - human

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Search completed: June 3, 2005, 09:17:51 Job time: 8.09576 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 3, 2005, 08:31:37; Search time 32.7497 Seconds (without alignments) 1782.523 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-791-619-12 625 1 BVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVWGQG 114

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	ot ic	homod	homo	homo	homo	homo	homo	homo	mus	Cai	homo	pomo	homo	homo	homo	homo	mus	homo	homo	homo												
	Description	Q6pja4	Q9u190	Q9u172	Q8wuk1	Q9u171	Q65zc9	Q6in78	Q6gmy2	Q6pi81	09u193	Q6n089	Q6mzv7	Q9u191	P01768	Q9y509	Q6gmx2	696569	P01766	9nzm9Ö	P01793	P19181	06mzq6	Q8wu38	Q8nc16	Q8n5k4	Q9hcc1	P01764	Q99m22	Q96k68	P01767	P01771
	ID	Q6PJA4	06TD6Ö	Q9UL72	QBWUK1	Q9UL71	Q652C9	Q61N78	Q6GMY2	Q6P181	Q9UL93	Q6N089	D6MZV7	Q9UL91	HV3G_HUMAN	09Y509	Q6GMX2	Q96BB9	HV3E_HUMAN	Q6MZŪ6	HV24_MOUSE	HV05_CARAU	O6MZQ6	Q8WU38	QBNCL6	Q8N5K4	Q9HCC1	HV3C HUMAN	Q99M <u>2</u> 2	Q96K68	HV3F_HUMAN	HV3J HUMAN
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do	Query Match	6.59	9.59	64.6	64.1	64.0	64.0	64.0	63.8	63.5	63.2	63.2	63.1	63.0	62.8	62.8	62.7	62.7	62.6	62.6	62.4	62.0	62.0	62.0	61.4	61.4	61.4	61.3	9.09	9.09	0.09	0.09
	Score	412	410	403.5	400.5	400	400	400	398.5	397	395	395	394.5	393.5	392.5	392.5	392	392	391	391	390	387.5	387.5	387.5	384	m	383.5	383	37	378.5	375	375
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HV22_MOUSE	HV37 MOUSE	ŏezv <u>x</u> o	HV3I HUMAN	Q99KA4	Q80ZI7	HV23 MOUSE	HV46 MOUSE	Qelbūs	Q6PJ95	HV21 MOUSE	Q6P6C4	Q6M2V6	Q920E7
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123	119	487	119	487	487	123	137	136	544	122	465	479	119
0.09	59.9	59.8	59.5	59.4	59.4	59.2	59.2	59.1	59.0	58.8	58.8	58.8	58.7
375	374.5	373.5	372	371.5	371	370	370	369.5	368.5	367.5	367.5	367.5	367
32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

O6PJA4 ID O AC O	A4 PRELIMINARY; PRT; 470 AA. Q6PJA4 PRELIMINARY; PRT; 470 AA. G6PJA4; GTEMBLrel. 27, Created) O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
SEAS	(Trimblication of the control of the
88	0) 11
× ×	NCBI_TaxID=9606; [1]
R P	SEQUENCE FROM N.A. TISSUE=Primary B-Cells;
X g	MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899; Grandbarg D.T. Beingold R.B. Grange J. H. Derge J. G.
\$ \$	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Honking B. F. Jordan H. Morre T. May S.T. Wang J. Heigh F.
5	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA 6	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
¥.	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Z:	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
\$ \$	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Villalon D.K., Muznv D.M., Soderoren E.J., Lu X., Gibbs R.A.,
æ	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A a	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
5 5	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
R R	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15.000 full-lenoth human
RT	and mouse cDNA sequences.";
RL	c. Natl
Z :	[2]
R R	SEQUENCE FROM N.A. TISSUE=Primary B-Cells:
RA	Strausberg R.;
12 E	Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
š	P01861: 1ADO.
DR	ro; IPR003599;
DR	IPR007110;
8 B	InterPro; IPR003597; Ig.cl.
ž	IPR003596;
DR.	7654; C1-set
8 G	SWART; SM00409; IG; 2.
ä	SM00406; I
Z S	PROSITE; PS50835; IG_LIKE; 4.
ś	(NIT) (NIT)

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SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
Strausberg R.;
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NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                            20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSS-YWMSWVRQAPGKGLEWVANIKQDGSEKY
                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY
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                                                                                                                                                                                                                                           61 N-PSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCAR-GSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                             65.6%; Score 410; DB 2; Length 113;
71.3%; Pred. No. 3.2e-33;
tive 9; Mismatches 14; Indels 10; Gaps
                                                                                                           4; Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
MUX X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                            65.9%; Score 412; DB 2; Length 470; 72.4%; Pred. No. 9.5e-33; tive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035024; AAD56260.1; -.
HSSP; P01772; 2F84.
InterPro: IPR007110; Ig-like.
InterPro: IPR00556; Ig_v.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                             113 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
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NON TER
SEQUENCE
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Matches
                                                                                                         Matches
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ID QS
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ODT O11
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DDE O12
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TISSUB-PINARY B-Cells;

MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mobrins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninor P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Nichards S., Worley K.C., Hale S., Garcia A.M., Gab N.H., Gab,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Moriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"The staple of the sequences "T." "The staple of "T." "The staple of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BVQLVESGGGLVQPGGSLRLSCAASGFTVSSNY-MMWVRQAPGKGLESV-SVTYSGGSSY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAFYYCARDR--FGEFLFDYWGQG 1111
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
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Pred. No. 1.5e-32;
9; Mismatches 17; Indels 5
SEQUENCE FROM N.A. MEDICAL BOLL 1006/clin.1998.4531; MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wux X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035042; AADS6278.1; -.
PIR; S21205; S21205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P01783, IIGC.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.6%;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Conservative
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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN- 59
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TISSUB-Peripheral Nervous System;

TISSUB-Peripheral Nervous System;

MEDLINE-22388257; Pubmed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.0%; Score 400; DB 2; Length 240;
69.2%; Pred. No. 7.2e-32;
ive 12; Mismatches 14; Indels 10; Gaps
                                      60 YADSVKGRPTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRFDIWGQG 114
   60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
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"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL, Y13056; CAA73499.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.
                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C1g/7;
MEDLINE=97362799; PubMed=9219263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
NON_TER 1 240
SEQUENCE 240 AA; 25569 MW;
                                                                                                                                                                                                                                                                                                                                                                             Single-chain Fv (Fragment).
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Matches 81; Conservative
                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                      RESULT 6
Q652C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-----DWSEGVETFDIWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSS-YGMHWVRQAPGKGLEWVAVISYDGSNKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.1%; Score 400.5; DB 2; Length 613; 67.5%; Pred. No. 1.8e-31; rative 11; Mismatches 15; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databages. EMBL; BC020240; AAH20240.1; -. PIR; F36005; P36005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; S.
PROSITE; SS00290; IG MHC; UNKNOWN 3.
SRQUENCE 613 AA; 67295 MW; 60C7P5950671E315 CRC64;
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InterPro; IPR07110; Ig-like.
InterPro; IPR03596; Ig_v.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01861; 1ADQ.
Pfam; PF07654; C1-set; 4.
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                                                                                                                   PH1642; PH1642.
PH1643; PH1643.
PH1645; PH1645.
PH1646; PH1646.
PL0098; PL0098.
                                                                                                                                                                                                                                                                                                                                                                      S31119; S31119.
S70442; S70442.
                                                                                                                                                                                                                                                                                                         S15590; S15590.
S31116; S31116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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PIR;
PIR;
PIR;
PIR;
PIR;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci D., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McKernan K.J., Malek, J.A., Canarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Banchez A., Matchan B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.,
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TISSUE=Primary B-Cells,

MEDLINE=2238657; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGNYVV---PAAPWGQG 129
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 64.0%; Score 400; DB 2; Length 466; Best Local Similarity 69.3%; Pred. No. 1.5e-31; Matches 79; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50853 MW; 53E80BCEDE81076E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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HSSP; P01861; 1AD0.
InterPro; IPR003159; Ig.
InterPro; IPR003109; Ig-11ke.
InterPro; IPR003109; Ig C1.
InterPro; IPR003597; Ig WHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig V.
Pfam; PP07654; C1-6et; 3.
SWART; SW00407; IGC1; 3.
SWART; SW00407; IGC1; 3.
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60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-------YFGHW 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QVQLVESGGGLVKPGGSLRLSCAASGFTF-SDYYMSWIRQAPGKGLEWVSYISSSSSYTN 78
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 606;
                                                                                                                                                                                                                                                                                                                                                                  C TISSUE=Primary B-Cells;
C TISSUE=Primary B-Cells;
A Strausberg R.;
A Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
B MEL; BC073758; AH73758.1; -.
R InterPro; IPR001599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
R InterPro; IPR003597; Ig.cl.
R InterPro; IPR003596; Ig.w.
R InterPro; IPR003596; Ig.w.
R Pfam; PP07654; Cl.set; 4.
R Pfam; PP07654; Cl.set; 4.
R Pfam; PR00407; Ig.; 4.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 1Cv; 1.
R PROSITE; PS50835; IG LIKE; 5.
R PROSITE; PS50299; IG LIKE; 5.
R PROSITE; PS50299; IG LIKE; 5.
R PROSITE; PS50299; IG LIKE; 5.
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Pred. No. 2.8e-31;
Transpare 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein... SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                    cDNA sequences."
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 GMDVWGQG 146
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Best Local Similarity
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78; Conservative
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         HSSP; P01772; 2FB4.
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Q6MZV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 YVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTWTTVNADYY-YFYMDV 137
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YMNSWVRQAPGKGLEWVANIKQDGSEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.",
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MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 397; DB 2; Length 478;
65.3%; Pred. No. 3.1e-31;
ive 15; Mismatches 16; Indels
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N-MAY-2000 (TrEMBLrel. 13, Last sequence update).
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                         Strauberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041037; AAH41037.1; -.
HSSP; P010661; IADQ.
InterPro; IPR003599; IG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;
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EMBL, ARO35021, AAD56257.1; -.
FIR; PH1644; PH1644.
PIR; PL0120; PL0120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00710; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_W.
Pfam; PP07654; C1-8et; 3.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
HYDOLIE; PS50835; IG_LIKE; 4.
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nes 81; Conservative
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                                                                                                                                                                                                                                                                                                           TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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OC Bukar
OC Mamma
OC Bukar
OC MAMMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EVQLVESGGGLVQPGRSLRLSCAASGFTF-DDYAMHWVRQAPGKGLEWVSGISWNSGSIA 78
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                                                                                                                                                                                                                                                                                                          2 VOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Human rectum tumor;
TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
A Wambutt R., Heubner D., Mews H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
L. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
B. RBMEL; BX640627; CAE45781.1; -..
R RBMEL; BX640627; CAE45781.1; -..
R RSSP; PO1861; 1ADO.
R InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
R RART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R RROSITE; PS00359; IG_LIKE; 4.
R RROSITE; PS003290; IG_MIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGG----GGLGLGYWGQG 109
                                                                                                                                                                                                                                                                                                                                                                                                                61 NPSVKGRITISRDDSKATFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 472;
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66.7%; Pred. No. 4.8e-31;
ive 16; Mismatches 19; Indels
                                                                                                                                                                                                  Ouery Match 63.2%; Score 395; DB 2; Length 11 Best Local Similarity 70.2%; Pred. No. 1e-31; Matches 80; Conservative 10; Mismatches 18; Indels
il protein.
472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name-DKTZp6686P15220.
Name-DKTZp686F15220.
Name-DKTZp686F15220.
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Hypothetical protein DKFZp686C11235.

NCBI_TaxID=9606;

EMBL; BX640853; CAE45920.1; HSSP; P01861; 1ADQ.

PRT;

PRELIMINARY;

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1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGST-- 58
                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKGLEWV---SYISSTII 56
                                                                                                                                                                                                                                                                                                                                                  59 --NYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                        57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGD---SSEAFDIWGQG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NP-SVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQG 114
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                                                                                                                                                                                                                      11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lehnan D.W., Putnam F.W.,
"Amino acid sequence of the variable region of a human mu chain:
"Acid of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                         DB 2; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig-like.
Pyrrolidone carboxylic acid
                                                                                       1
118 118
118 AA; 12843 MW; D0633949F2AC149D CRC64;
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122 AA, 13668 MW, A42D0F17D252F1C2 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient with macroglobulinemia.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02051; M3HUAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                      63.0%; Score 393.5; DB 2
69.5%; Pred. No. 1.5e-31;
iive 9; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
Ig heavy chain V-III region CAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-V.
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InterPro, IPR007110; Ig-11ke.
InterPro, IPR003596; Ig-v.
SMRAT; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                             Local Similarity 69.5
les 82, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 EIQLVESGGGLVQPGGSLRLSCAASGPTFSS-FEMIWVRQAPGKGLEWLSYITRSGNTVY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWH---PAVWGQG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
TISSUE-Human small intestine;
The German Human cDNA Consortium;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035023; AAD56259.1; -.
PIR; PH0875; PH0875.
PIR; S21205; S21205.
PIR; S30531; S30531.
HSSP; P01783; 11GC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.1%; Score 394.5; DB 2; Length 473; Best Local Similarity 64.4%; Pred. No. 5.4e-31; Matches 76; Conservative 18; Mismatches 19; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MW X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig-like.
InterPro; IPR003006; Ig-did.
InterPro; IPR003596; Ig-Mic.
InterPro; IPR003596; Ig-Mic.
InterPro; IPR003596; Ig-Mic.
InterPro; IPR003596; Ig-Mic.
InterPro; IPR00409; Ig-Mic.
InterPro; IPR00409; Ig-Mic.
InterPro; IPR00409; Ig-Mic.
IPR051TE; SM00406; IGV; I.
IPROSITE; PS00299; Ig-Mic. UNKNOWN_2.
IPROSITE; PS00299; Ig-Mic. UNKNOWN_2.
IPROSITE; PS00299; Ig-Mic. UNKNOWN_2.
IPROCHECIAL Protein.
IPROCHECIAL PROTEIN.
                  Q6MZV7;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
  473 AA.
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PRELIMINARY;

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RESULT 13

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NCBI_TaxID=9606;

(Fragment)

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RESULT 15

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No. 11 Control of the Control of Control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVHLVESGGGVVQPGKSLRLSCEASGFTF-STYGMSWVRQAPGKGLDWVALISYDGSTQY 59
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                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.8%; Score 392.5; DB 2; Length 147; Best Local Similarity 65.0%; Pred. No. 2.4e-31; Matches 78; Conservative 15; Mismatches 20; Indels 7.
                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH3 protein (Fragment).
                                    147 AA
                                    PRT;
                                PRELIMINARY;
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